SEQ. ID. NO.:1

GAGACTGCAGCAGAATATGTAAAATCTCGACTCCCAGAGGCTCTTAAGC AGCACCTTCAGGATTATGAGAAGGACAAAGAAAACAGTGTTCTGACCTA CCAGACCATCCTCGAGCAGCAGATCTTGTCAATTGACCGGGAAATGCTG GAAAAGTTGACAGTCTCCTATGATGAAGCAGGCACAACGTGTTTGATCS CTCTACTCTCAGATAAAGACCTCACCGTGGCCAACGTTGGTGACTCTCG GGGAGTCTTGTGTGACAAAGATGGCAATGCCATCCCCTTGTCTCACGAT CACAAGCCTTACCAGCTGAAGGAAAGGAAGAGGATAAAGAGAGCTGGTG GGTTCATCAGCTTTAATGGCTCCTGGAGGGTCCAGGGAATCCTAGCCAT GTCTCGATCCCTGGGAGACTATCCACTGAAAAATCTCAACGTGGTCATC CCAGACCCAGACATCTTGACCTTTGACCTGGACAAGCTGCAGCCGGAGT TCATGATCTTGGCCTCAGATGGCCTGTGGGATGCTTTCAGCAATGAAGA AGCGGTTCGATTCATCAAGGAGCGCTTGGATGAGCCCCACTTTGGGGCC AAAAGCATCGTCCTGCAGTCCTTTTACAGAGGCTGCCCTGACAACATCA CTGTCATGGTGGTGAAGTTCAGGAATAGTAGCAAAACAGAAGAGCACTG AACCCTGCCAGATCTCAGCTGCCCCAAACTAGAGGACTCTCAACATACT GTTCTCTTCATGTAGTAAAAGGTGTGGGTATAATTAGGATCATGCGTCC CAACAGAACCCCCTTCCCTGATGGCCTTGAATCCCTTTGGAGTACTG AGCAGAGGGTTGGTTCCCTTGCTGACACCGCAGAGGCTGCTAAGTTTGT CAGATCCCACATATGAGGCAAAGGAAAGGCAGGCCATATGTTTTCCTTC TTAATAATGTACTTTT

SEQ. ID. NO.:2

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1.3

ETAAEYVKSRLPEALKQHLQDYEKDKENSVLTYQTILEQQILSIDREML EKLTVSYDEAGTTCLIXLLSDKDLTVANVGDSRGVLCDKDGNAIPLSHD HKPYQLKERKRIKRAGGFISFNGSWRVQGILAMSRSLGDYPLKNLNVVI PDPDILTFDLDKLQPEFMILASDGLWDAFSNEEAVRFIKERLDEPHFGA KSIVLQSFYRGCPDNITVMVVKFRNSSKTEEH

FIGURE 1

<u>Underlined</u> = deleted in targeting construct **Bold** = sequence flanking Neo insert in targeting construct

GAGACTGCAGCAGAATATGTAAAATCTCGACTCCCAGAGGCTCTTAAGCAGCACCTTCAG GATTATGAGAAGGACAAAGAAAACAGTGTTCTGACCTACCAGACCATCCTCGAGCAGCAG ATCTTGTCAATTGACCGGGAAATGCTGGAAAAGTTGACAGTCTCCTATGATGAAGCAGGC ACAACGTGTTTGATCSCTCTACTCTCAGATAAAGACCTCACCGTGGCCAACGTTGGTGAC TCTCGGGGAGTCTTGTGTGACAAAGATGGCAATGCCATCCCCTTGTCTCACGATCACAAG CCTTACCAGCTGAAGGAAAGGAAGAGATAAAGAGAGCTGGTGGGTTCATCAGCTTTAAT GGCTCCTGGAGGGTCCAGGGAATCCTAGCCATGTCTCGATCCCTGGGAGACTATCCACTG AAAAATCTCAACGTGGTCATCCCAGACCCAGACATCTTGACCTTTGACCTGGACAAGCTG CAGCCGGAGTTCATGATCTTGGCCTCAGATGGCCTGTGGGATGCTTTCAGCAATGAAGA AGCGGTTCGATTCATCAAGGAGCGCTTGGATGAGCCCCACTTTGGGGCCCAAAAGCA**TCGT** CCTGCAGTCCTTTTACAGAGGCTGCCCTGACAACATCACTGTCATGGTGGTGAAGTTCAG GAATAGTAGCAAAACAGAAGAGCACTGAACCCTGCCAGATCTCAGCTGCCCCAAACTAGA GGACTCTCAACATACTGTTCTCTTCATGTAGTAAAAGGTGTGGGTATAATTAGGATCATG CGTCCCAACACAGAACCCCCTTCCCTGATGGCCTTGAATCCCTTTGGAGTACTGAGCAGA GGGTTGGTTCCCTTGCTGACACCGCAGAGGCTGCTAAGTTTGTGTCCCCCCAGCCCTTCT ATCAGTGTTTGAAACACATACGTAGGTAGCCACAGATCCCACATATGAGGCAAAGGAAAG GCAGGCCATATGTTTTCCTTCTTAATAATGTACTTTT

FIGURE 2A